

# 11  
5/8/02

1600

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/667,380A

DATE: 05/02/2002  
 TIME: 17:21:26

Input Set : A:\LEX-0042-USA SEQLIST.txt  
 Output Set: N:\CRF3\05022002\I667380A.raw

ENTERED

4 <110> APPLICANT: Donoho, Gregory  
 5 Turner, C. Alexander Jr.  
 6 Wattler, Frank  
 7 Nehls, Michael  
 8 Friedrich, Glenn  
 9 Zambrowicz, Brian  
 10 Sands, Arthur T.  
 12 <120> TITLE OF INVENTION: Novel Human Protease Inhibitor-Like  
 13 Proteins and Polynucleotides Encoding the Same  
 16 <130> FILE REFERENCE: LEX-0042-USA  
 C--> 18 <140> CURRENT APPLICATION NUMBER: US/09/667,380A  
 C--> 18 <141> CURRENT FILING DATE: 2000-09-22  
 18 <150> PRIOR APPLICATION NUMBER: US 60/156,101  
 19 <151> PRIOR FILING DATE: 1999-09-24  
 21 <160> NUMBER OF SEQ ID NOS: 3  
 23 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 25 <210> SEQ ID NO: 1  
 26 <211> LENGTH: 1491  
 27 <212> TYPE: DNA  
 28 <213> ORGANISM: homo sapiens  
 30 <400> SEQUENCE: 1

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32 caaggctacc	tcctgcccac	cgtcactctc	ttagaggagc	tgctcagcaa	ataccagcac	120
33 aacgagctct	actcccgggt	ccgcagagcc	atccccagg	aggacaagga	ggagatccct	180
34 atgctgcaca	acaagcttcg	gggcccagg	cagcctcagg	cctccaacat	ggagtacatg	240
35 acctgggtag	acgaactgga	gaagtctgct	gcagcgtggg	ccagtcagtg	catctgggag	300
36 caccggcccc	ccagtctgct	ggtgtccatc	gggcagaacc	tgggcgctca	ctggggcagg	360
37 tatcgctctc	cgggggtcca	tgtgcagtc	tggtatgacg	aggtgaagga	ctacacctac	420
38 ccctaccgga	gcgagtgcaa	cccctgggtg	ccagagaggt	gctcggggcc	tatgtgcacg	480
39 cactacacac	agatagtttg	ggccaccacc	aacaagatcg	gttggtgctg	gaacacctgc	540
40 cggaagatga	ctgtctgggg	agaagtttgg	gagaacgcgg	tctactttgt	ctgcaattat	600
41 tctccaaagg	ggaactggat	tggagaagcc	ccctacaaga	atggccggcc	ctgctctgag	660
42 tgccccacca	gctatggagg	cagctgcagg	aacaacttgt	gttaccgaga	agaaacctac	720
43 actccaaaac	ctgaaacgga	cgagatgaat	gaggtggaaa	cggctcccat	tcctgaagaa	780
44 aaccatgttt	ggctccaacc	gaggggtgat	agaccaccca	agcccaagaa	aacctctgcg	840
45 gtcaactaca	tgacccaagt	cgtcagatgt	gacaccaaga	tgaaggacag	gtgcaaaggg	900
46 tccacgtgta	acaggtacca	gtgcccagca	ggctgcctga	accacaaggc	gaagatcttt	960
47 ggaagtctgt	tctatgaaag	ctcgtctagc	atatgcgcgc	ccgccatcca	ctacgggatc	1020
48 ctggatgaca	agggaggcct	ggtggatctc	accaggaacg	ggaaggtccc	cttcttcgtg	1080
49 aagtctgaga	gacacggcgt	gcagtccttc	agcaaataca	aaccttccag	ctcattcatg	1140
50 gtgtcaaaaag	tgaaagtgca	ggatttggac	tgctacacga	ccgttgctca	gctgtgcccg	1200
51 tttgaaaagc	cagcaactca	ctgcccaga	atccattgtc	cggcacactg	caaagacgaa	1260
52 ccttcctact	gggctccggg	gtttggaacc	aacatctatg	cagatacctc	aagcatctgc	1320

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53 aagacagctg tgcacgcggg agtcatcagc aacgagagtg ggggtgacgt ggacgtgatg 1380
54 cccgtggata aaaagaagac ctacgtgggc tcgctcagga atggagttca gtctgaaagc 1440
55 ctggggactc ctcgggatgg aaaggccttc cggatctttg ctgtcaggca g 1491
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58 <211> LENGTH: 497
59 <212> TYPE: PRT
60 <213> ORGANISM: homo sapiens
62 <400> SEQUENCE: 2
63 Met Ser Cys Val Leu Gly Gly Val Ile Pro Leu Gly Leu Leu Phe Leu
64 1 5 10 15
65 Val Cys Gly Ser Gln Gly Tyr Leu Leu Pro Asn Val Thr Leu Leu Glu
66 20 25 30
67 Glu Leu Leu Ser Lys Tyr Gln His Asn Glu Ser His Ser Arg Val Arg
68 35 40 45
69 Arg Ala Ile Pro Arg Glu Asp Lys Glu Glu Ile Leu Met Leu His Asn
70 50 55 60
71 Lys Leu Arg Gly Gln Val Gln Pro Gln Ala Ser Asn Met Glu Tyr Met
72 65 70 75 80
73 Thr Trp Asp Asp Glu Leu Glu Lys Ser Ala Ala Ala Trp Ala Ser Gln
74 85 90 95
75 Cys Ile Trp Glu His Gly Pro Thr Ser Leu Leu Val Ser Ile Gly Gln
76 100 105 110
77 Asn Leu Gly Ala His Trp Gly Arg Tyr Arg Ser Pro Gly Phe His Val
78 115 120 125
79 Gln Ser Trp Tyr Asp Glu Val Lys Asp Tyr Thr Tyr Pro Tyr Pro Ser
80 130 135 140
81 Glu Cys Asn Pro Trp Cys Pro Glu Arg Cys Ser Gly Pro Met Cys Thr
82 145 150 155 160
83 His Tyr Thr Gln Ile Val Trp Ala Thr Thr Asn Lys Ile Gly Cys Ala
84 165 170 175
85 Val Asn Thr Cys Arg Lys Met Thr Val Trp Gly Glu Val Trp Glu Asn
86 180 185 190
87 Ala Val Tyr Phe Val Cys Asn Tyr Ser Pro Lys Gly Asn Trp Ile Gly
88 195 200 205
89 Glu Ala Pro Tyr Lys Asn Gly Arg Pro Cys Ser Glu Cys Pro Pro Ser
90 210 215 220
91 Tyr Gly Gly Ser Cys Arg Asn Asn Leu Cys Tyr Arg Glu Glu Thr Tyr
92 225 230 235 240
93 Thr Pro Lys Pro Glu Thr Asp Glu Met Asn Glu Val Glu Thr Ala Pro
94 245 250 255
95 Ile Pro Glu Glu Asn His Val Trp Leu Gln Pro Arg Val Met Arg Pro
96 260 265 270
97 Thr Lys Pro Lys Lys Thr Ser Ala Val Asn Tyr Met Thr Gln Val Val
98 275 280 285
99 Arg Cys Asp Thr Lys Met Lys Asp Arg Cys Lys Gly Ser Thr Cys Asn
100 290 295 300
101 Arg Tyr Gln Cys Pro Ala Gly Cys Leu Asn His Lys Ala Lys Ile Phe
102 305 310 315 320
103 Gly Ser Leu Phe Tyr Glu Ser Ser Ser Ser Ile Cys Arg Ala Ala Ile

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104                               325                               330                               335
105 His Tyr Gly Ile Leu Asp Asp Lys Gly Gly Leu Val Asp Ile Thr Arg
106                               340                               345                               350
107 Asn Gly Lys Val Pro Phe Phe Val Lys Ser Glu Arg His Gly Val Gln
108                               355                               360                               365
109 Ser Leu Ser Lys Tyr Lys Pro Ser Ser Ser Phe Met Val Ser Lys Val
110                               370                               375                               380
111 Lys Val Gln Asp Leu Asp Cys Tyr Thr Thr Val Ala Gln Leu Cys Pro
112 385                               390                               395                               400
113 Phe Glu Lys Pro Ala Thr His Cys Pro Arg Ile His Cys Pro Ala His
114                               405                               410                               415
115 Cys Lys Asp Glu Pro Ser Tyr Trp Ala Pro Val Phe Gly Thr Asn Ile
116                               420                               425                               430
117 Tyr Ala Asp Thr Ser Ser Ile Cys Lys Thr Ala Val His Ala Gly Val
118                               435                               440                               445
119 Ile Ser Asn Glu Ser Gly Gly Asp Val Asp Val Met Pro Val Asp Lys
120                               450                               455                               460
121 Lys Lys Thr Tyr Val Gly Ser Leu Arg Asn Gly Val Gln Ser Glu Ser
122 465                               470                               475                               480
123 Leu Gly Thr Pro Arg Asp Gly Lys Ala Phe Arg Ile Phe Ala Val Arg
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125 Gln
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129 <211> LENGTH: 2272
130 <212> TYPE: DNA
131 <213> ORGANISM: homo sapiens
133 <400> SEQUENCE: 3
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136 ggtgattgga gccctgcgga gagctcaagc gccagctctt gcccsaggag cccagggctgc 180
137 cccgtgagtc ccatagttgc tgcaggagt gagccatgag ctgctgcctg ggtggtgtca 240
138 tccccctggg gctgctgttc ctggtctgcg gatcccaagg ctacctctctg cccaacgtca 300
139 ctctcttaga ggagctgctc agcaaatacc agcacaacga gtctcactcc cgggtccgca 360
140 gagccatccc caggaggagc aaggaggaga tcctcatgct gcacaacaag cttcggggcc 420
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142 ctgctgcagc gtgggccagt cagtgcattt gggagcacgg gccaccagt ctgctggtgt 540
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145 ggtgtccaga gaggtgctcg gggcctatgt gcacgcacta cacacagata gtttgggcca 720
146 ccaccaacaa gatcggttgt gctgtgaaca cctgccggaa gatgactgtc tggggagaag 780
147 tttgggagaa cgcggtctac tttgtctgca attattctcc aaaggggaac tggattggag 840
148 aagcccccta caagaatggc cgccctgct ctgagtcccc acccagctat ggaggcagct 900
149 gcaggaacaa cttgtgttac cgagaagaaa cctacactcc aaaacctgaa acggacgaga 960
150 tgaatgaggt ggaacaggct cccattcctg aagaaaacca tgtttggtc caaccgaggg 1020
151 tgatgagacc caccaagccc aagaaaacct ctgcggtcaa ctacatgacc caagtcgtca 1080
152 gatgtgacac caagatgaag gacagggtga aagggtccac gtgtaacagg taccagtgcc 1140
153 cagcaggctg cctgaaccac aaggcgaaga tctttggaag tctgtttat gaaagctcgt 1200
154 ctacgatatg ccgcgccgcc atccactacg ggatcctgga tgacaaggga ggccgtggtg 1260
155 atatcaccag gaacgggaag gtccccttct tcgtgaagtc tgagagacac ggctgtgagc 1320

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156	ccctcagcaa	atacaaacct	tccagctcat	tcatggtgtc	aaaagtgaaa	gtgcaggatt	1380
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158	caagaatcca	ttgtccggca	cactgcaaag	acgaaccttc	ctactgggct	ccggtgtttg	1500
159	gaaccaacat	ctatgcagat	acctcaagca	tctgcaagac	agctgtgcac	gcgggagtc	1560
160	tcagcaacga	gagtgggggt	gacgtggacg	tgatgcccgt	ggataaaaag	aagacctacg	1620
161	tggtctcgt	caggaatgga	gttcagtctg	aaagcctggg	gactcctcgg	gatggaaagg	1680
162	ccttccggat	ctttgctgtc	aggcagtga	tttccagcac	caggggagaa	ggggcgtctt	1740
163	caggagggt	tcggggtttt	gcttttattt	ttattttgtc	attgcggggt	atatggagag	1800
164	tcaggaaact	tcctttgact	gatgttcagt	gtccatcact	ttgtggcctg	tgggtgaggt	1860
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166	gcctgatcct	gctggggcct	gggggtctcc	atctggacgt	cctctctcct	ttagagatct	1980
167	gagctgtctc	ttaaagggga	cagttgcca	aaatgttcct	tgctatgtgt	tcttctgttg	2040
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VERIFICATION SUMMARY

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Input Set : A:\LEX-0042-USA SEQLIST.txt  
Output Set: N:\CRF3\05022002\I667380A.raw

L:18 M:270 C: Current Application Number differs, Replaced Current Application No  
L:18 M:271 C: Current Filing Date differs, Replaced Current Filing Date